

## SEQUENCE SUBMISSION

SEQ ID NO: 1 is a primate HDTEA84 nucleic acid sequence.  
SEQ ID NO: 2 is a primate HDTEA84 amino acid sequence.  
5 SEQ ID NO: 3 is a primate HSLJD37R nucleic acid sequence.  
SEQ ID NO: 4 is a primate HSLJD37R amino acid sequence.  
SEQ ID NO: 5 is supplemented primate HSLJD37R nucleic acid sequence.  
SEQ ID NO: 6 is supplemented primate HSLJD37R amino acid sequence.  
10 SEQ ID NO: 7 is variant primate HSLJD37R nucleic acid sequence.  
SEQ ID NO: 8 is variant primate HSLJD37R amino acid sequence.  
SEQ ID NO: 9 is murine TNF-R2 amino acid sequence.  
SEQ ID NO: 10 is human TNF-R2 amino acid sequence.  
SEQ ID NO: 11 is human OPG amino acid sequence.  
15 SEQ ID NO: 12 is a rodent RANKL nucleic acid sequence.  
SEQ ID NO: 13 is a rodent RANKL amino acid sequence.  
SEQ ID NO: 14 is a primate RANKL nucleic acid sequence.  
SEQ ID NO: 15 is a primate RANKL amino acid sequence.  
SEQ ID NO: 16 is another primate RANKL nucleic acid sequence.  
20 SEQ ID NO: 17 is another primate RANKL amino acid sequence.  
SEQ ID NO: 18 is a variant primate RANKL nucleic acid sequence.  
SEQ ID NO: 19 is a variant primate RANKL amino acid sequence.

<110> Murphy, Erin E.  
Mattson, Jeanine D.  
25 Bates, Elizabeth Esther Mary  
Gorman, Daniel M.  
Lebecque, Serge J.E.

<120> Mammalian Genes; Related Reagents

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<sup>15</sup> See, for example, the 1990s book, *Women and Work: A Feminist Perspective* by Linda H. Hays (1990).

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90		-35	-30

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Ile	Ala	Arg	Arg	Ala	Thr	Ala	Thr	Met	Ile	Ala	Gly	Ser	Leu	Leu	Leu		
-25					-20				-15						-10		
5	ctt	gga	ttc	ctt	agc	acc	acc	aca	gct	cag	eca	gaa	cag	aag	gcc	tcg	144
	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	Lys	Ala	Ser	
					-5				-1	1				5			
10	aat	ctc	att	ggc	aca	tac	cgc	cat	gtt	gac	cgt	gcc	acc	ggc	cag	gtg	192
	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	Thr	Gly	Gln	Val	
					10				15				20				
15	cta	acc	tgt	gac	aag	tgt	cca	gca	gga	acc	tat	gtc	tct	gag	cat	tgt	240
	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	Val	Ser	Glu	His	Cys	
					25				30				35				
20	acc	aac	aca	agc	ctg	cgc	gtc	tgc	agc	agt	tgc	cct	gtg	ggg	acc	ttt	288
	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	Cys	Pro	Val	Gly	Thr	Phe	
					40				45				50			55	
25	acc	agg	cat	gag	aat	ggc	ata	gag	aaa	tgc	cat	gac	tgt	agt	cag	cca	336
	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	Cys	His	Asp	Cys	Ser	Gln	Pro	
					60				65				70				
30	tgc	cca	tgg	cca	atg	att	gag	aaa	tta	cct	tgt	gct	gcc	ttg	act	gac	384
	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	
					75				80				85				
35	cga	gaa	tgc	act	tgc	cca	cct	ggc	atg	ttc	cag	tct	aac	gct	acc	tgt	432
	Arg	Glu	Cys	Thr	Cys	Pro	Pro	Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	
					90				95				100				
40	gcc	ccc	cat	acg	gtg	tgt	cct	gtg	ggt	tgg	ggt	gtg	cg	aaa	ggg	480	
	Ala	Pro	His	Thr	Val	Cys	Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	
					105				110				115				
45	aca	gag	act	gag	gat	gtg	cg	tgt	aag	cag	tgt	gct	cg	gg	acc	ttc	528
	Thr	Glu	Thr	Glu	Asp	Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	
					120				125				130			135	
50	tca	gat	gtg	cct	tct	agt	gtg	atg	aaa	tgc	aaa	gca	tac	aca	gac	tgt	576
	Ser	Asp	Val	Pro	Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	
					140				145				150				
55	ctg	agt	cag	aac	ctg	gtg	gtg	atc	aag	ccg	ggg	acc	aag	gag	aca	gac	624
	Leu	Ser	Gln	Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	
					155				160				165				
60	aac	gtc	tgt	ggc	aca	ctc	ccg	tcc	ttc	tcc	agc	tcc	acc	tca	cct	tcc	672
	Asn	Val	Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	
					170				175				180				
65	cct	ggc	aca	gcc	atc	ttt	cca	cgc	cct	gag	cac	atg	gaa	acc	cat	gaa	720
	Pro	Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
					185				190				195				
70	gtc	cct	tcc	tcc	act	tat	gtt	ccc	aaa	ggc	atg	aac	tca	aca	gaa	tcc	768
	Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	Ser	
					200				205				210			215	

aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa	816
Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu	
220 225 230	
5 ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa gac gtg	864
Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val	
235 240 245	
10 aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc	912
Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro	
250 255 260	
15 cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg	960
His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly	
265 270 275	
20 ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct	1008
Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro	
280 285 290 295	
25 aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg	1056
Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp	
300 305 310	
25 atg att gtg ctt ttc ctg ctg gtg ctt gtg gtg att gtg gtg tgc	1104
Met Ile Val Leu Phe Leu Leu Val Leu Val Val Ile Val Val Cys	
315 320 325	
30 agt atc cgg aaa agc tcg agg act ctg aaa aag ggg ccc cgg cag gat	1152
Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp	
330 335 340	
35 ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca	1200
Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro	
345 350 355	
40 acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat gga ccc	1248
Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro	
360 365 370 375	
45 cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat	1296
His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr	
380 385 390	
50 tacttcaccc tgggaggcag catagtgcag tgaaaggtat cgatatcctg aagctttag 1402	
cagcccaagt gggaaagccag tggaaagata tctatcgtt tctttgcaat gccagtgaga 1462	
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-40 -35 -305 Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu  
-25 -20 -15 -10Leu Gly Phe Leu Ser Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser  
-5 -1 1 510 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val  
10 15 2015 Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys  
25 30 35Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe  
40 45 50 5520 Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro  
60 65 70Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp  
75 80 8525 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys  
90 95 10030 Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly  
105 110 115Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe  
120 125 130 13535 Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys  
140 145 150Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp  
155 160 16540 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser  
170 175 18045 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
185 190 195Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser  
200 205 210 21550 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu  
220 225 230Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val  
235 240 24555 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro  
250 255 26060 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly  
265 270 275

Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro  
280 285 290 295

5 Arg Gln Asn Leu His His Phe Asp Ile Asn Glu His Leu Pro Trp  
300 305 310

Met Ile Val Leu Phe Leu Leu Val Leu Val Val Ile Val Val Cys  
315 320 325

10 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp  
330 335 340

15 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro  
345 350 355

Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro  
360 365 370 375

20 His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr  
380 385 390

Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly  
395 400

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30 <213> rodent

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35 Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr  
20 25 30

Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp  
40 35 40 45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val  
50 55 60

45 Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu  
65 70 75 80

Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser  
85 90 95

50 Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr  
100 105 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala  
55 115 120 125

Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys  
130 135 140

60 Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn

MURPHY, et al.

100

SF0818K

145 150 155 160

Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser  
165 170 175

5

Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile  
180 185 19010 Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr  
195 200 205Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr  
210 215 22015 Arg Ser Gln  
225

20 &lt;210&gt; 10

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; primate

25 &lt;400&gt; 10

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
1 5 10 15Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
20 25 30

30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
35 40 4535 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
50 55 60Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
65 70 75 80

40

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
85 90 95Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
100 105 110

45

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
115 120 125

50

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
130 135 140Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
145 150 155 160

55

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
165 170 175Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
180 185 190

60

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
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5 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
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Gln  
225

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20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
35 40 45

25 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
50 55 60

30 Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
85 90 95

35 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
115 120 125

40 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

45 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
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Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
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&lt;220&gt;

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5 &lt;222&gt; (191)..(553)

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Met Ala Leu Lys15 gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc cta 163  
Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu  
-25 -20 -15 -1020 ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg cag 211  
Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg Gln  
-5 -1 1 525 cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag tgc 259  
Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys  
10 15 2030 gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307  
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu  
25 30 3535 gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355  
Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp Trp  
40 45 50 5540 ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac cgc 403  
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg  
60 65 7045 ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg gac 451  
Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp  
75 80 8550 tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa gac 499  
Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp  
90 95 10055 atg gag tgt gtg ccc tgc gga gac cca cct ccc tac gaa cca cac 547  
Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Tyr Glu Pro His  
105 110 11560 tgt gag tgatgtgcc a gtggcagca gac tttaaa aaaaaaagaa aaaaaaacaa 603  
Cys Glu  
120

65 acaaaaacaa aaaaaaaaaa aaaaaaaaaa aaa 636

55

&lt;210&gt; 13

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; rodent

60

&lt;400&gt; 13

Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala  
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5 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly  
 -10 -5 -1 1

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu  
 5 10 15

10 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
 20 25 30 35

15 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe  
 40 45 50

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala  
 55 60 65

20 Leu, Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala  
 70 75 80

25 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
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Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro  
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30 Tyr Glu Pro His Cys Glu  
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&lt;210&gt; 14

&lt;211&gt; 474

35 <212> DNA

&lt;213&gt; primate

&lt;220&gt;

&lt;221&gt; CDS

40 <222> (78)...(473)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (308)

45 <223> N at 308, 315, 333, 412, 431, 436, 444, and 473 may be A, C, G, or  
 T; translated amino acid depends on genetic code

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ttaccggct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110  
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln  
 1 5 10

55 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158  
 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu  
 15 20 25

60 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206

	Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala			
	30	35	40	
5	tgc cct cct cgc agt aca aaa gca gct ggg gcc acc aca aat gtc aga			254
	Cys Pro Pro Arg Ser Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg			
	45	50	55	
10	gtt gca tca cct gtg ctg tca tca atc gtg ttc aga agg ttc aac tgc			302
	Val Ala Ser Pro Val Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys			
	60	65	70	75
	aca gtn acc tct nat gct gtc tgt ggg gga ngg ttt gcc caa gtt tct			350
	Thr Xaa Thr Ser Xaa Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser			
	80	85	90	
15	aac cga aag aca cgc cat tgg aag gct gcc agg acc aag gat ggc atc			398
	Asn Arg Lys Thr Arg His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile			
	95	100	105	
20	ccg tgg cac aaa gnc aga ccc cca act tct gan ggt tnc aaa gtg nct			446
	Pro Trp His Lys Xaa Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa			
	110	115	120	
25	ttc caa ttg gag ctt aat ggg agg can a			474
	Phe Gln Leu Glu Leu Asn Gly Arg Xaa			
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	<212> PRT			
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	20	25	30	
40	Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Ser			
	35	40	45	
45	Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg Val Ala Ser Pro Val			
	50	55	60	
	Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys Thr Xaa Thr Ser Xaa			
	65	70	75	80
50	Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser Asn Arg Lys Thr Arg			
	85	90	95	
	His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile Pro Trp His Lys Xaa			
	100	105	110	
55	Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa Phe Gln Leu Glu Leu			
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	Asn Gly Arg Xaa			
60	130			

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 and 541 may be A, C, G, or T  
  
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 ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa   110  
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln  
 1            5           10  
  
 25          tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta   158  
 Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu  
 15           20           25  
  
 30          tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc   206  
 Ser Lys Asp Cys Gly Tyr Gly Glu Gly Asp Ala Tyr Cys Thr Ala  
 30           35           40  
  
 35          tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag   254  
 Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln  
 45           50           55  
  
 40          agt tgc atc acc tgt gct atc aat cgt gtt cag aag gtc caa ctg   302  
 Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu  
 60           65           70           75  
  
 45          cac agc taacctctna tgctgtctgt gggatgttt gncccaagtt ctnaccgaaa   358  
 His Ser  
  
 50          agacacgcca tggaaaggct ggcaggacca ngtatggccn tccctggca gaaagccaga 418  
 cccccaacn nctgnaggtt ccaatgtggc cttncattt ggaagcttan tggaaaggca 478  
 gatgncaacc caaagtggcc cttcaggga ggcggaaatt tggatggcaat ggggtgnagca 538  
 gcttgcca   546  
  
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					20				25				30			
5	Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
					35				40			45				
10	Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
					50				55			60				
	Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Gln	Leu	His	Ser			
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	<211>	932														
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	<213>	primate														
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	<222>	(78) .. (770)														
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	<223>	N; may be A, C, G, or T														
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	Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln					
35						1			5			10				
	tgg	gga	cg	tg	tc	acc	tgc	caa	cg	tg	ct	gga	cag	gag	cta	158
	Trp	Gly	Arg	Cys	Val	Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu
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	Ser	Lys	Asp	Cys	Gly	Tyr	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala		
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	Ser	Cys	Ile	Thr	Cys	Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys
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	Thr	Ala	Ser	Asn	Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	
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	Arg	Lys	Thr	Arg	Ile	Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys
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Gln Gln Gln Gly Pro Glu Met  
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